

activity. Displays a preference for an acidic residue N-terminal to the isomerized proline bond. Catalyzing pSer/Thr-Pro cis/trans isomerizations.

-1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline (omega=0).

-1- SUBCELLULAR LOCATION: Nuclear.

-1- SIMILARITY: Belongs to the ppic/parvulin rotamase family.

-1- SIMILARITY: Contains 1 WW domain.

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DR ENBL; U49070; AAC50492.1; --

DR ENBL; BC002899; AAH02899.1; --

DR PIR; S68520; S68520.

DR PDB; 1F8A; X-ray; B=1-163.

DR PDB; 1I6C; NMR; A=6-44.

DR PDB; 1I8G; NMR; B=6-44.

DR PDB; 1I8H; NMR; B=6-44.

DR PDB; 1NMV; NMR; A=1-163.

DR PDB; 1NMW; NMR; A=50-163.

DR PDB; 1PIN; X-ray; A=1-163.

DR Genew; HGNC:8988; PIN1.

DR HInvDB; HIX0014730; --

DR MIM; 601052; --

DR GO; GO:0005634; C:nucleus; TAS.

DR GO; GO:0005515; F:protein binding; TAS.

DR GO; GO:0007088; P:regulation of mitosis; TAS.

DR InterPro; IPR000297; Rotamase.

DR InterPro; IPR01202; WW_Rep5_WWP.

DR Pfam; PF00639; Rotamase; 1.

DR Pfam; PF00397; WW; 1.

DR SMART; SM00456; WW; 1.

DR PROSITE; PS01096; PPIC_PPIASE_1; 1.

DR PROSITE; PS01098; PPIC_PPIASE_2; 1.

DR PROSITE; PS01159; WW_DOMAIN_1; 1.

DR PROSITE; PS00020; WW_DOMAIN_2; 1.

DR 3D-structure; Cell cycle; Isomerase; Nuclear protein; Rotamase.

FT DOMAIN 5 39

FT DOMAIN 52 163

FT TURN 9 10

FT STRAND 11 15

FT TURN 17 18

FT STRAND 22 26

FT TURN 27 29

FT STRAND 32 33

FT STRAND 55 62

FT TURN 65 66

FT STRAND 72 72

FT TURN 73 74

FT STRAND 75 75

FT TURN 82 98

FT HELIX 99 99

FT TURN 103 110

FT HELIX 114 118

FT TURN 119 120

FT STRAND 121 125

FT TURN 127 128

FT HELIX 132 140

FT TURN 143 144

FT STRAND 146 146

FT STRAND 150 151

FT STRAND 155 161

SQ SEQUENCE 163 AA; 18243 MW; 35391AF40B7D1E13 CRC64;

Query Match 100.0%; Score 534; DB 1; Length 163;

Seq-Local Similarity 100.0%; Pred. No. 7.9e-46;

Seq-Id 100%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Apr 15 16:09:52 2005

QY 1 HLLVKHSRRPSSWRQEKITRTKEEALELINGYIOIKSGEEDFESLASOFCSSAKA 60

DB 59 HLLVKHSRRPSSWRQEKITRTKEEALELINGYIOIKSGEEDFESLASOFCSSAKA 118

QY 61 RGDLCAPSRGQWQKPFEDASPALRTGEMSGPVTDSGHIILRTE 105

DB 119 RGDLCAPSRGQWQKPFEDASPALRTGEMSGPVTDSGHIILRTE 163

RESULT 2

ID PIN1 MOUSE STANDARD; PRT; 165 AA.

AC Q9QUR7;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE 05-JUL-2004 (Rel. 44, Last annotation update)

DE Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (EC 5.2.1.8)

DE (Rotamase Ptnl) (PPIase Ptnl).

GN Name=Ptnl;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=20070807; PubMed=10600477; DOI=10.1006/bbrc.1999.1736;

RP Fujimori F., Takanashi K., Uchida C., Uchida T.;

RP "Mice lacking Ptnl develop normally, but are defective in entering cell cycle from G0 arrest.";

RL Biochem. Biophys. Res. Commun. 265:658-663(1999).

RN [2]

RP SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=Embryo, and Kidney;

RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01286;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka H., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.

RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kongsaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Sempole C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

CC -1- FUNCTION: Essential PPIase that regulates mitosis presumably by interacting with NIMA and attenuating its mitosis-promoting activity. Displays a preference for an acidic residue N-terminal to the isomerized proline bond. Catalyzing pSer/Thr-Pro cis/trans isomerizations (By similarity).

CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline (omega=0).

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -1- SIMILARITY: Belongs to the ppic/parvulin rotamase family.

Exhibit C

CC -!- SIMILARITY: Contains 1 WW domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
CC
CC EMBL; AB009691; BAA87037.1; -
CC EMBL; AB009692; BAA87038.1; -
CC EMBL; AK003369; BAB22743.1; -
CC EMBL; AK002665; BAB22270.1; -
CC PIR; JC7136; JC7136.
CC HSP; Q13526; 1F8A.
CC MGD; MG11346036; Pnl.
CC GO; GO:0042127; P:regulation of cell proliferation; IMP.
CC InterPro; IPR00297; Rotamase.
CC InterPro; IPR001202; WW_Rp5_WWP.
CC Pfam; PF00639; Rotamase; 1.
CC Pfam; PF00397; WW; 1.
CC SMART; SM00456; WW; 1.
CC PROSITE; PS01096; PPIC_PPIASE_1; 1.
CC PROSITE; PS01198; PPIC_PPIASE_2; 1.
CC PROSITE; PS01159; WW_DOMAIN_1; 1.
CC PROSITE; PS00020; WW_DOMAIN_2; 1.
CC Cell cycle; Isomerase; Nuclear protein; Rotamase.
KW DOMAIN 5 39 WW
FT DOMAIN 54 165 PpIC.
SQ SEQUENCE 165 AA; 18370 MW; 18895F009176B1F CRC64;

Query Match 98.3%; Score 525; DB 1; Length 165;
Best Local Similarity 98.1%; Pred. No. 6.5e-45;
Matches 103; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLLVKSQSRPPSSWRQEKITRTKEALELINGYIQKISGEDEFESLASQSDCSAKA 60
DB 61 HLLVKSQSRPPSSWRQEKITRTKEALELINGYIQKISGEDEFESLASQSDCSAKA 120

QY 61 RGLGAFSGQKQKPEDASFAALRTGEMSGPVFTDSGIHILRTE 165
DB 121 RGLGAFSGQKQKPEDASFAALRTGEMSGPVFTDSGIHILRTE 165

RESULT 3
QAZRS ID Q6AZR5 PRELIMINARY; PRT; 158 AA.
AC Q6AZR5; 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein (fragment)
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RT Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX PubMed=1477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Klein S., Strausberg R., to the EMBL/GenBank/DBJ databases.
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the PpIC/parvulin rotamase family.
CC EMBL; BC077447; AAH77447.1; -
CC GO; GO:0016853; F:isomerase activity; IEA.
CC InterPro; IPR000297; Rotamase.
CC InterPro; IPR002349; WW_Rp5_WWP.
CC InterPro; IPR001202; WW_Rp5_WWP.
CC Pfam; PF00639; Rotamase; 1.
CC Pfam; PF00397; WW; 1.
CC PRINTS; PR00403; WWDOMAIN.
CC SMART; SM00456; WW; 1.
CC PROSITE; PS01096; PPIC_PPIASE_1; 1.
CC PROSITE; PS01198; PPIC_PPIASE_2; 1.
CC PROSITE; PS01159; WW_DOMAIN_1; 1.
CC PROSITE; PS00020; WW_DOMAIN_2; 1.
CC Hypothetical protein; Isomerase; Rotamase.
KW NON_TER 1
FT SEQUENCE 158 AA; 17339 MW; EB94FF9F7650FFA1 CRC64;

Query Match 91.0%; Score 486; DB 2; Length 158;
Best Local Similarity 88.6%; Pred. No. 5.3e-41;
Matches 93; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 1 HLLVKSQSRPPSSWRQEKITRTKEALELINGYIQKISGEDEFESLASQSDCSAKA 60
DB 54 HLLVKSQSRPPSSWRQEKITRTKEALELINGYIQKISGEDEFESLASQSDCSAKA 113

QY 61 RGLGAFSGQKQKPEDASFAALRTGEMSGPVFTDSGIHILRTE 105
DB 114 RGLGAFSGQKQKPEDASFAALRTGEMSGPVFTDSGIHILRTE 158

RESULT 4
Q919K6 ID Q919K6 PRELIMINARY; PRT; 159 AA.
AC Q919K6; 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Prolyl isomerase Pnl.
GN Name=Pnl.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20165035; PubMed=10698738; DOI=10.1126/science.287.5458.1644;
RA Winkler K.E., Swenson K.I., Kornbluth S., Means A.R.;
RT "Requirement of the prolyl isomerase Pnl for the replication